

# REPLACEMENT SHEET

Figure 1A

```
# Aligned_sequences: 2
# 1: Pcan057
# 2: Pcan057v1
# Matrix: EDNAFULL
# Gap_penalty: 100.0
# Extend_penalty: 0.05
#=====
```

Pcan057	1	aaacttcatcaagggtacntaagggttgtaagggttctcggggggtagcggct	50
Pcan057v1	1		0
Pcan057	51	tgcacacctcttgaagggttcarccgggccctggctccttcaggctgg	100
Pcan057v1	1		0
Pcan057	101	ctgccttnatccgcttatccaatgattggataacggatgaggggagtcctg	150
Pcan057v1	1		0
Pcan057	151	ggtgccagggtgctttgcccgcattggcccatcagtcacgctgcagtcct	200
Pcan057v1	1		0
Pcan057	201	gtcaggaaaaaatcagtggtattctcattctacatatgagaaaactgagg	250
Pcan057v1	1		0
Pcan057	251	cttgcagatataagggccaaaagttacacagctagtgagtgatggggctg	300
Pcan057v1	1		0
Pcan057	301	agtttcagactccacagtctcttaaccaccaagcagcatgccagagtag	350
Pcan057v1	1		0
Pcan057	351	aggtgagaaggaaggagagagctgcgggtccacatgagcatctggacctag	400
Pcan057v1	1		0
Pcan057	401	catggacaactcactcctccctggctctcgcctttgttcttggtgcgggtg	450
Pcan057v1	1		0
Pcan057	451	tggtggtggtgggactcaaagacggtaaagatagctttctctcctccctg	500
Pcan057v1	1		0
Pcan057	501	gggaatctgggggttggtttaaaaggcctgctcctcttttagaaggcagga	550
Pcan057v1	1		0

# REPLACEMENT SHEET

Figure 1B

Pcan057	551	gggcccccaaggaagcagaagggtgacagaaggggaaagggtcctctgatc	600
Pcan057v1	1		0
Pcan057	601	attgctc-----	607
Pcan057v1	1	<div> <div>   </div> <div> . </div> <div>   </div> <div> . </div> <div>   </div> <div>   </div> <div>   </div> <div>   </div> </div> aattctcgcgagctcgtcgaccggtcgacgagctcgagggtcgacgagctcg	50
Pcan057	608	-----	607
Pcan057v1	51	agggcgcgcgccccggccccccacccctcgcagcaccccgcgccccgcgccc	100
Pcan057	608	-----	607
Pcan057v1	101	tcccagccgggtccagccggagccatggggccggagccgcagtgcagcacc	150
Pcan057	608	-----	607
Pcan057v1	151	atggagctggcggccttggtgccgctgggggctcctcctcgccctcttgcc	200
Pcan057	608	-----	607
Pcan057v1	201	ccccggagccgcgcgagcacccaagtgtgcaccggcacagacatgaagctgc	250
Pcan057	608	-----	607
Pcan057v1	251	ggctccctgccagtcccgcagacccacctggacatgctccgccacctctac	300
Pcan057	608	-----	607
Pcan057v1	301	cagggctgccaggtggtgcagggaaacctggaactcacctacctgcccac	350
Pcan057	608	-----	607
Pcan057v1	351	caatgccagcctgtccttcctgcaggatatccaggaggtgcagggctacg	400
Pcan057	608	-----	607
Pcan057v1	401	tgctcatcgctcacaaccaagtgaggcaggtcccactgcagaggctgcgg	450
Pcan057	608	-----	607
Pcan057v1	451	attgtgcgaggcacccagctctttgaggacaactatgccctggccgtgct	500
Pcan057	608	-----	607
Pcan057v1	501	agacaatggagacccgctgaacaataccaccctgtcacaggggcctccc	550

# REPLACEMENT SHEET

Figure 1C

Pcan057	608	-----acccacagagatcttgaaa	627
		.   .	
Pcan057v1	51	caggaggcctgcgggagctgcagcttcgaagcctcacagagatcttgaaa	600
Pcan057	628	ggaggggtcttgatccagcggaacccccagctctgctaccaggacacgat	677
Pcan057v1	601	ggaggggtcttgatccagcggaacccccagctctgctaccaggacacgat	650
Pcan057	678	tttgtggaaggacatcttccacaagaacaaccagctggctctcacactga	727
Pcan057v1	651	tttgtggaaggacatcttccacaagaacaaccagctggctctcacactga	700
Pcan057	728	tagacaccaaccgctctcgggctgccacccctgttctccgatgtgtaag	777
Pcan057v1	701	tagacaccaaccgctctcgggctgccacccctgttctccgatgtgtaag	750
Pcan057	778	ggctcccgtgctggggagagagttctgaggattgtcagagcctgacgcg	827
Pcan057v1	751	ggctcccgtgctggggagagagttctgaggattgtcagagcctgacgcg	800
Pcan057	828	cactgtctgtgccggtggctgtgccgctgcaagggggccactgccactg	877
Pcan057v1	801	cactgtctgtgccggtggctgtgccgctgcaagggggccactgccactg	850
Pcan057	878	actgctgccatgagcagtgtgctgccggctgcacggggccccaagcactct	927
Pcan057v1	851	actgctgccatgagcagtgtgctgccggctgcacggggccccaagcactct	900
Pcan057	928	gactgcctggcctgcctccacttcaaccacagtggcatctgtgagctgca	977
Pcan057v1	901	gactgcctggcctgcctccacttcaaccacagtggcatctgtgagctgca	950
Pcan057	978	ctgcccagccctggtcacctacaacacagacacgtttgagtccatgcca	1027
Pcan057v1	951	ctgcccagccctggtcacctacaacacagacacgtttgagtccatgcca	1000
Pcan057	1028	atcccaggggcccgtatacattcggcgccagctgtgtgactgcctgtccc	1077
Pcan057v1	1001	atcccaggggcccgtatacattcggcgccagctgtgtgactgcctgtccc	1050
Pcan057	1078	tacaactacctttctacggacgtgggatcctgcaccctcgctctgccccct	1127
Pcan057v1	1051	tacaactacctttctacggacgtgggatcctgcaccctcgctctgccccct	1100
Pcan057	1128	gcacaaccaagaggtgacagcagaggatggaacacagcggtgtgagaagt	1177
Pcan057v1	1101	gcacaaccaagaggtgacagcagaggatggaacacagcggtgtgagaagt	1150
Pcan057	1178	gcagcaagccctgtgcccagagtgtgctatggctctgggcatggagcacttg	1227
Pcan057v1	1151	gcagcaagccctgtgcccagagtgtgctatggctctgggcatggagcacttg	1200

# REPLACEMENT SHEET

Figure 1D

Pcan057	1228	cgagaggtgagggcagttaccagtgccaatatccaggagtttgctggctg	1277
Pcan057v1	1201	cgagaggtgagggcagttaccagtgccaatatccaggagtttgctggctg	1250
Pcan057	1278	caagaagatctttgggagcctggcatttctgccggagagccttgatgggg	1327
Pcan057v1	1251	caagaagatctttgggagcctggcatttctgccggagagccttgatgggg	1300
Pcan057	1328	accagcctccaacactgccccgctccagccagagcagctccaagtgttt	1377
Pcan057v1	1301	accagcctccaacactgccccgctccagccagagcagctccaagtgttt	1350
Pcan057	1378	gagactctggaagagatcacaggttacctatacatctcagcatggccgga	1427
Pcan057v1	1351	gagactctggaagagatcacaggttacctatacatctcagcatggccgga	1400
Pcan057	1428	cagcctgcctgacctcagcgtcttccagaacctgcaagtaatccggggac	1477
Pcan057v1	1401	cagcctgcctgacctcagcgtcttccagaacctgcaagtaatccggggac	1450
Pcan057	1478	gaattctgcacaatggcgctactcgtgaccctgcaagggctgggcatc	1527
Pcan057v1	1451	gaattctgcacaatggcgctactcgtgaccctgcaagggctgggcatc	1500
Pcan057	1528	agctggctggggctgcgctcactgaggggaactgggcagtggactggccct	1577
Pcan057v1	1501	agctggctggggctgcgctcactgaggggaactgggcagtggactggccct	1550
Pcan057	1578	catccaccataaacacccacctctgcttcgtgacacgggtgccctgggacc	1627
Pcan057v1	1551	catccaccataaacacccacctctgcttcgtgacacgggtgccctgggacc	1600
Pcan057	1628	agctctttcgggaacccgcaccaagctctgctccacactgccaaccggcca	1677
Pcan057v1	1601	agctctttcgggaacccgcaccaagctctgctccacactgccaaccggcca	1650
Pcan057	1678	gaggacgagtg-----	1689
Pcan057v1	1651	gaggacgagtggtgtaagacagggagcccagtggtgcgcactccccatctg	1700
Pcan057	1690	-----	1689
Pcan057v1	1701	ccagcacacagcagtgcccagggggccctggcagcagcgttcttgactt	1750
Pcan057	1690	-----	1689
Pcan057v1	1751	gtgcagactgcccgtctctgtgcacccttcttgactcagcacagctctgg	1800
Pcan057	1690	-----	1689

# REPLACEMENT SHEET

**Figure 1E**

Pcan057v1	1801	ctggcttggcctcttggcatggcttctctagctgggtcctacctgccttg	1850
Pcan057	1690	-----	1689
Pcan057v1	1851	gcataccttccctccccctctgtttctgaaatctcagaactcttccctctcc	1900
Pcan057	1690	-----	1689
Pcan057v1	1901	ctacatcggccccacctgtccccaccctccagccccacagccatgcccac	1950
Pcan057	1690	-----	1689
Pcan057v1	1951	agccagttccctgggttcacttggacctggggcctccccctaaaagtccct	2000
Pcan057	1690	-----gtgggcgagggcctggcctgccaccag	1716
Pcan057v1	2001	gcggtcccttccctcctcactgcagtgggcgagggcctggcctgccaccag	2050
Pcan057	1717	ctgtgcgccccgagggcactgctgggggtccagggcccaccagtggtgtcaa	1766
Pcan057v1	2051	ctgtgcgccccgagggcactgctgggggtccagggcccaccagtggtgtcaa	2100
Pcan057	1767	ctgcagccagttccttcggggccaggagtgcgtggaggaatgccgagtac	1816
Pcan057v1	2101	ctgcagccagttccttcggggccaggagtgcgtggaggaatgccgagtac	2150
Pcan057	1817	tgcaggggctccccagggagtatgtgaatgccaggcactgtttgccgtgc	1866
Pcan057v1	2151	tgcaggggctccccagggagtatgtgaatgccaggcactgtttgccgtgc	2200
Pcan057	1867	caccctgagtgtcagccccagaatggctcagtgacctgttttgaccgga	1916
Pcan057v1	2201	caccctgagtgtcagccccagaatggctcagtgacctgttttgaccgga	2250
Pcan057	1917	ggctgaccagtggtgtggcctgtgcccactataaggaccctcccttctgcg	1966
Pcan057v1	2251	ggctgaccagtggtgtggcctgtgcccactataaggaccctcccttctgcg	2300
Pcan057	1967	tggcccgtgccccagcgggtgtgaaacctgacctctcctacatgccatc	2016
Pcan057v1	2301	tggcccgtgccccagcgggtgtgaaacctgacctctcctacatgccatc	2350
Pcan057	2017	tggaagtttccagatgaggagggcgcatgccagccttgccccatcaactg	2066
Pcan057v1	2351	tggaagtttccagatgaggagggcgcatgccagccttgccccatcaactg	2400
Pcan057	2067	caccactcctgtgtggacctggatgacaagggctgccccgccgagcaga	2116
Pcan057v1	2401	caccactcctgtgtggacctggatgacaagggctgccccgccgagcaga	2450

# REPLACEMENT SHEET

Figure 1F

Pcan057	2117	gagccagccctctgacgtccatcatctctgcggtggttggcattctgctg	2166
Pcan057v1	2451	gagccagccctctgacgtccatcatctctgcggtggttggcattctgctg	2500
Pcan057	2167	gtcgtggtccttgggggtggtctttgggatcctcatcaagcgacggcagca	2216
Pcan057v1	2501	gtcgtggtccttgggggtggtctttgggatcctcatcaagcgacggcagca	2550
Pcan057	2217	gaagatccggaagtacacgatgaggagactgctgcaggaaacggagctgg	2266
Pcan057v1	2551	gaagatccggaagtacacgatgaggagactgctgcaggaaacggagctgg	2600
Pcan057	2267	tggagccgctgacacctagcggagcgcgatgcccaaccaggcgcagatgcgg	2316
Pcan057v1	2601	tggagccgctgacacctagcggagcgcgatgcccaaccaggcgcagatgcgg	2650
Pcan057	2317	atcctgaaagagacggagctgaggaaggtgaaggtgcttggatctggcgc	2366
Pcan057v1	2651	atcctgaaagagacggagctgaggaaggtgaaggtgcttggatctggcgc	2700
Pcan057	2367	ttttggcacagtctacaagggcatctggatccctgatggggagaatgtga	2416
Pcan057v1	2701	ttttggcacagtctacaagggcatctggatccctgatggggagaatgtga	2750
Pcan057	2417	aaattccagtgggccatcaaagtgttgagggaaaacacatccccaaagcc	2466
Pcan057v1	2751	aaattccagtgggccatcaaagtgttgagggaaaacacatccccaaagcc	2800
Pcan057	2467	aacaaagaaatcttagacgaagcatacgtgatggctgggtgtgggctcccc	2516
Pcan057v1	2801	aacaaagaaatcttagacgaagcatacgtgatggctgggtgtgggctcccc	2850
Pcan057	2517	atatgtctcccgcttctgggcatctgcctgacatccacgggtgcagctgg	2566
Pcan057v1	2851	atatgtctcccgcttctgggcatctgcctgacatccacgggtgcagctgg	2900
Pcan057	2567	tgacacagcttatgccctatggctgcctcttagaccatgtccgggaaaac	2616
Pcan057v1	2901	tgacacagcttatgccctatggctgcctcttagaccatgtccgggaaaac	2950
Pcan057	2617	cgcggaagcctgggctcccaggacctgctgaactgggtgtatgcagattgc	2666
Pcan057v	2951	cgcggaagcctgggctcccaggacctgctgaactgggtgtatgcagattgc	3000
Pcan057	2667	caaggggatgagctacctggaggatgtgcggctcgctacacagggaacttg	2716
Pcan057v1	3001	caaggggatgagctacctggaggatgtgcggctcgctacacagggaacttg	3050

# REPLACEMENT SHEET

Figure 1G

Pcan057	2717	ccgctcggaacgtgctggtcaagagtcccaaccatgtcaaaattacagac	2766
Pcan057v1	3051	ccgctcggaacgtgctggtcaagagtcccaaccatgtcaaaattacagac	3100
Pcan057	2767	ttcgggctggctcggtgctggacattgacgagacagagtaccatgcaga	2816
Pcan057v1	3101	ttcgggctggctcggtgctggacattgacgagacagagtaccatgcaga	3150
Pcan057	2817	tgggggcaaggtgcccacatcaagtggatggcgctggagtccattctccgcc	2866
Pcan057v1	3151	tgggggcaaggtgcccacatcaagtggatggcgctggagtccattctccgcc	3200
Pcan057	2867	ggcgggttcaccaccagagtgatgtgtggagtattggtgtgactgtgtgg	2916
Pcan057v1	3201	ggcgggttcaccaccagagtgatgtgtggagtattggtgtgactgtgtgg	3250
Pcan057	2917	gagctgatgacttttggggccaaaccttacgatgggatcccagcccggga	2966
Pcan057v1	3251	gagctgatgacttttggggccaaaccttacgatgggatcccagcccggga	3300
Pcan057	2967	gatccctgacctgctggaaaagggggagcggctgccccagcccccatct	3016
Pcan057v1	3301	gatccctgacctgctggaaaagggggagcggctgccccagcccccatct	3350
Pcan057	3017	gcaccattgatgtctacatgatcatggtcaaagtgttgatgattgactct	3066
Pcan057v1	3351	gcaccattgatgtctacatgatcatggtcaaagtgttgatgattgactct	3400
Pcan057	3067	gaatgtcggccaagattccgggagttggtgtctgaattctcccgcattggc	3116
Pcan057v1	3401	gaatgtcggccaagattccgggagttggtgtctgaattctcccgcattggc	3450
Pcan057	3117	cagggacccccagcgctttgtggtcatccagaatgaggacttggggccag	3166
Pcan057v1	3451	cagggacccccagcgctttgtggtcatccagaatgaggacttggggccag	3500
Pcan057	3167	ccagtcaccttggaacagcaccttctaccgctcactgctggaggacgatgac	3216
Pcan057v1	3501	ccagtcaccttggaacagcaccttctaccgctcactgctggaggacgatgac	3550
Pcan057	3217	atgggggacctggtggatgctgaggagtatctggtaccccagcagggtt	3266
Pcan057v1	3551	atgggggacctggtggatgctgaggagtatctggtaccccagcagggtt	3600
Pcan057	3267	cttctgtccagacctgccccgggcgctgggggcatggtccaccacaggc	3316
Pcan057v1	3601	cttctgtccagacctgccccgggcgctgggggcatggtccaccacaggc	3650
Pcan057	3317	accgcagctcatctaccaggagtggcggtggggacctgacactagggctg	3366
Pcan057v1	3651	accgcagctcatctaccaggagtggcggtggggacctgacactagggctg	3700

# REPLACEMENT SHEET

Figure 1H

Pcan057	3367	gagccctctgaagaggaggccccaggtctccactggcaccctccgaagg	3416
Pcan057v1	3701	gagccctctgaagaggaggccccaggtctccactggcaccctccgaagg	3750
Pcan057	3417	ggctggctccgatgtatttgatgggtgacctgggaatgggggcagccaagg	3466
Pcan057v1	3751	ggctggctccgatgtatttgatgggtgacctgggaatgggggcagccaagg	3800
Pcan057	3467	ggctgcaaagcctccccacacatgaccccagccctctacagcggtacagt	3516
Pcan057v1	3801	ggctgcaaagcctccccacacatgaccccagccctctacagcggtacagt	3850
Pcan057	3517	gaggacccccacagtaccctgcctctgagactgatggctacgttgcccc	3566
Pcan057v1	3851	gaggacccccacagtaccctgcctctgagactgatggctacgttgcccc	3900
Pcan057	3567	cctgacctgcagccccagcctgaatatgtgaaccagccagatgttcggc	3616
Pcan057v1	3901	cctgacctgcagccccagcctgaatatgtgaaccagccagatgttcggc	3950
Pcan057	3617	cccagcccccttcgccccgagagggccctctgcctgctgccgacctgct	3666
Pcan057v1	3951	cccagcccccttcgccccgagagggccctctgcctgctgccgacctgct	4000
Pcan057	3667	ggtgccactctggaaagggccaagactctctccccaggggaagaatgggg	3716
Pcan057v1	4001	ggtgccactctggaaagggccaagactctctccccaggggaagaatgggg	4050
Pcan057	3717	cgtcaaagacgtttttgcctttgggggtgccgtggagaacccccgagtact	3766
Pcan057v1	4051	cgtcaaagacgtttttgcctttgggggtgccgtggagaacccccgagtact	4100
Pcan057	3767	tgacacccccagggaggagctgcccctcagccccaccctcctcctgccttc	3816
Pcan057v1	4101	tgacacccccagggaggagctgcccctcagccccaccctcctcctgccttc	4150
Pcan057	3817	agcccagccttcgacaacctctattactgggaccaggaccaccagagcg	3866
Pcan057v1	4151	agcccagccttcgacaacctctattactgggaccaggaccaccagagcg	4200
Pcan057	3867	gggggctccaccagcaccttcaaagggacacctacggcagagaacccag	3916
Pcan057v1	4201	gggggctccaccagcaccttcaaagggacacctacggcagagaacccag	4250
Pcan057	3917	agtacctgggtctggacgtgccagtgtgaaccagaaggccaagtccgcag	3966
Pcan057v1	4251	agtacctgggtctggacgtgccagtgtgaaccagaaggccaagtccgcag	4300
Pcan057	3967	aagccctgatgtgtcctcagggagcaggggaaggcctgacttctgctggca	4016
Pcan057v1	4301	aagccctgatgtgtcctcagggagcaggggaaggcctgacttctgctggca	4350



# REPLACEMENT SHEET

Figure 11

Pcan057	4017	tcaagaggtgggagggccctccgaccacttccaggggaacctgccatgcc	4066
Pcan057v1	4351	tcaagaggtgggagggccctccgaccacttccaggggaacctgccatgcc	4400
Pcan057	4067	aggaacctgtcctaaggaaccttccttcctgcttgagttcccagatggct	4116
Pcan057v1	4401	aggaacctgtcctaaggaaccttccttcctgcttgagttcccagatggct	4450
Pcan057	4117	ggaaggggtccagcctcggttggaagaggaacagcactggggagtctttgt	4166
Pcan057v1	4451	ggaaggggtccagcctcggttggaagaggaacagcactggggagtctttgt	4500
Pcan057	4167	ggattctgaggccctgcccaatgagactctaggggtccagtggatgccaca	4216
Pcan057v1	4501	ggattctgaggccctgcccaatgagactctaggggtccagtggatgccaca	4550
Pcan057	4217	gccagcttgggccctttccttcagatcctgggtactgaaagccttaggg	4266
Pcan057v1	4551	gccagcttgggccctttccttcagatcctgggtactgaaagccttaggg	4600
Pcan057	4267	aagctggcctgagaggggaagcgccctaaggagtggtctaagaacaaaa	4316
Pcan057v1	4601	aagctggcctgagaggggaagcgccctaaggagtggtctaagaacaaaa	4650
Pcan057	4317	gcgacccattcagagactgtccctgaaacctagtactgcccccatgagg	4366
Pcan057v1	4651	gcgacccattcagagactgtccctgaaacctagtactgcccccatgagg	4700
Pcan057	4367	aaggaacagcaatgggtgtcagtatccaggctttgtacagagtgcttttct	4416
Pcan057v1	4701	aaggaacagcaatgggtgtcagtatccaggctttgtacagagtgcttttct	4750
Pcan057	4417	gtttagtttttacttttttgttttgttttttaaatgaaataaagac	4466
Pcan057v1	4751	gtttagtttttacttttttgttttgttttttaaatgaaataaagac	4800
Pcan057	4467	ccaggggggagaatgggtgttgatggggaggcaagtgtggggggtccttc	4516
Pcan057v1	4801	ccaggggggagaatgggtgttgatggggaggcaagtgtggggggtccttc	4850
Pcan057	4517	tccacacccacttttgtccatttgcaaatatattttggaaaaca	4559
Pcan057v1	4851	tccacacccacttttgtccatttgcaaatatattttggaaaaca	4893

# REPLACEMENT SHEET

Figure 2A

```
# Aligned_sequences: 2
# 1: Pcan057.aa
# 2: Pcan057v1.aa
# Matrix: EBLSUM62
# Gap_penalty: 100.0
# Extend_penalty: 0.01
#=====

Pcan057.aa      1                                     0

Pcan057v1.aa    1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPEHLDMRLHLY 50

Pcan057.aa      1                                     0

Pcan057v1.aa    51 QGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLR 100

Pcan057.aa      1                                     MGLSFRHLHSLLTTKQ 15
                                     .....:|.||
Pcan057v1.aa    101 IVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSL----- 145

Pcan057.aa      16 HAQSRGEKEGESCGPHEHLDLAWTTHSSLALALFLLRVWWWDSTVKIA 65

Pcan057v1.aa    146 ----- 145

Pcan057.aa      66 FSPPWGIWGLFKRPAPLLEGRRAPREAEGDRRGKGPLIIAHPTEILKGGV 115
                                     |||||
Pcan057v1.aa    146 -----TEILKGGV 153

Pcan057.aa      116 LIQRNPQLCYQDTILWKDIFHKNNQLALTIDTNRSRACHPCSPMCKGSR 165
      |||||
Pcan057v1.aa    154 LIQRNPQLCYQDTILWKDIFHKNNQLALTIDTNRSRACHPCSPMCKGSR 203

Pcan057.aa      166 CWGESSEDCQSLTRTVCAAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCL 215
      |||||
Pcan057v1.aa    204 CWGESSEDCQSLTRTVCAAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCL 253

Pcan057.aa      216 ACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYN 265
      |||||
Pcan057v1.aa    254 ACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYN 303

Pcan057.aa      266 LSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREV 315
      |||||
Pcan057v1.aa    304 LSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREV 353

Pcan057.aa      316 RAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETL 365
      |||||
Pcan057v1.aa    354 RAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETL 403
```

1111

1

## REPLACEMENT SHEET

Figure 2C

Pcan057v1.aa	576			575
Pcan057.aa	1016	SGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPT		1065
Pcan057v1.aa	576			575
Pcan057.aa	1066	HDPSPQLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPR		1115
Pcan057v1.aa	576			575
Pcan057.aa	1116	EGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGA		1165
Pcan057v1.aa	576			575
Pcan057.aa	1166	APQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDV		1215
Pcan057v1.aa	576			575
Pcan057.aa	1216	PV	1217	
Pcan057v1.aa	576		575	

# REPLACEMENT SHEET

Figure 3A

```
# Aligned_sequences: 2
# 1: Pro108
# 2: Pro177
# Matrix: EDNAFULL
# Gap_penalty: 100.0
# Extend_penalty: 0.01
#=====

Pro108      1                                     gcacga      6
                                     ...|..
Pro177      1 gggagggataggacggggagacaaagaaaggggtgcggcagcactgccag      50

Pro108      7 ggggaagaggggtgatccgacccggggaaggtcgctgggcagggcgagttgg      56
          |||
Pro177     51 ggggaagaggggtgatccgacccggggaaggtcgctgggcagggcgagttgg      100
          |||

Pro108     57 gaaagcggcagccccgcgcgcgcgcgcagccccttctcctcctttctccc      106
          |||
Pro177    101 gaaagcggcagccccgcgcgcgcgcgcagccccttctcctcctttctccc      150
          |||

Pro108    107 acgtcctatctgcctctcgctggaggccaggccgctgcagcatcgaagaca      156
          |||
Pro177    151 acgtcctatctgcctctcgctggaggccaggccgctgcagcatcgaagaca      200
          |||

Pro108    157 ggaggaactggagcctcattggccggcccgggcgccggcctcgggctta      206
          |||
Pro177    201 ggaggaactggagcctcattggccggcccgggcgccggcctcgggctta      250
          |||

Pro108    207 aataggagctccgggctctggctgggacccgaccgctgccggccgcgctc      256
          |||
Pro177    251 aataggagctccgggctctggctgggacccgaccgctgccggccgcgctc      300
          |||

Pro108    257 ccgctgctcctgccgggtgatggaaaacccagcccggccgcccctgg      306
          |||
Pro177    301 ccgctgctcctgccgggtgatggaaaacccagcccggccgcccctgg      350
          |||

Pro108    307 gcaaggccctctgcgctctcctcctggccactctcggcgccgcccggccag      356
          |||
Pro177    351 gcaaggccctctgcgctctcctcctggccactctcggcgccgcccggccag      400
          |||

Pro108    357 cctcttgggggagagtccatctgttccgccagagccccggccaaatacag      406
          |||
Pro177    401 cctcttgggggagagtccatctgttccgccagagccccggccaaatacag      450
          |||

Pro108    407 catcaccttcacgggcaagtggagccagacggccttccccaagcagtacc      456
          |||
Pro177    451 catcaccttcacgggcaagtggagccagacggccttccccaagcagtacc      500
          |||

Pro108    457 ccctgttccgccccctgcgcagtggtcttcgctgctgggggcccgcgat      506
          |||
```

# REPLACEMENT SHEET

Figure 3B

Pro177	501	ccctgttccgccccccctgcgcagtggtcttcgctgctgggggcccgcgc	550
Pro108	507	agctccgactacagcatgtggaggaagaaccagtacgtcagtaacgggct	556
Pro177	551	agctccgactacagcatgtggaggaagaaccagtacgtcagtaacgggct	600
Pro108	557	gcgcgactttgcgagcgcggcgaggcctgggcgctgatgaaggagatcg	606
Pro177	601	gcgcgactttgcgagcgcggcgaggcctgggcgctgatgaaggagatcg	650
Pro108	607	aggcgggcgggggaggcgctgcagagcgtgcacgcggtgttttcggcgccc	656
Pro177	651	aggcgggcgggggaggcgctgcagagcgtgcacgaggtgttttcggcgccc	700
Pro108	657	gccgtccccagcggcaccgggcagacgtcggcgagctggaggtgcagcg	706
Pro177	701	gccgtccccagcggcaccgggcagacgtcggcgagctggaggtgcagcg	750
Pro108	707	caggcactcgctgggtctcgtttgtggtgcgcacgtgcccagccccgact	756
Pro177	751	caggcactcgctgggtctcgtttgtggtgcgcacgtgcccagccccgact	800
Pro108	757	ggttcgtgggcgtggacagcctggacctgtgcgacggggaccgttggcgg	806
Pro177	801	ggttcgtgggcgtggacagcctggacctgtgcgacggggaccgttggcgg	850
Pro108	807	gaacaggcgggcgctggacctgtaccctacgacgccgggacggacagcgg	856
Pro177	851	gaacaggcgggcgctggacctgtaccctacgacgccgggacggacagcgg	900
Pro108	857	cttcaccttctcctcccccaacttcgccaccatcccgcaggacacgggtga	906
Pro177	901	cttcaccttctcctcccccaacttcgccaccatcccgcaggacacgggtga	950
Pro108	907	ccgagataacgtcctcctctcccagccaccggccaactccttctactac	956
Pro177	951	ccgagataacgtcctcctctcccagccaccggccaactccttctactac	1000
Pro108	957	ccgcggctgaaggccctgcctcccatcgccaggggtgacactggtgcggct	1006
Pro177	1001	ccgcggctgaaggccctgcctcccatcgccaggggtgacactgctgcggct	1050
Pro108	1007	gcgacagagccccagggccttcacccctcccggcccagtcctgccagca	1056
Pro177	1051	gcgacagagccccagggccttcacccctcccggcccagtcctgccagca	1100
Pro108	1057	gggacaatgagattgtagacagcgcct-----	1083
Pro177	1101	gggacaatgagattgtagacagcgcctcaggtaacggacatacaggtcac	1150

# REPLACEMENT SHEET

Figure 3C

Pro108	1084	-----	1083
Pro177	1151	atgggacacacagcagccccgaaccctgccacagggcgaccaccaaacc	1200
Pro108	1084	-----	1083
Pro177	1201	gaacctaaggctctgagaaattccaagtagggattcgtagtgcgactgc	1250
Pro108	1084	-----	1083
Pro177	1251	aagatgggtgcctagaagatttaggattctgttgattcacacactgaagat	1300
Pro108	1084	-----	1083
Pro177	1301	gtgactcttgccacattatttgagttgaaagcatcttacagggccacagc	1350
Pro108	1084	-----	1083
Pro177	1351	ccagaggaaagaatgaaaggaggctccagacagtacctgagagactctgt	1400
Pro108	1084	-----	1083
Pro177	1401	cctgtcagacacgcacccacaggtgacctgtgtgtcacagctgacaagga	1450
Pro108	1084	-----	1083
Pro177	1451	agcttgctaggatggccctgtgtggccaccgggtgacagctatgctgcag	1500
Pro108	1084	-----	1083
Pro177	1501	ggcacctgtgggggtctcgggaccagccaccacacagctcggggctctg	1550
Pro108	1084	-----	1083
Pro177	1551	ctcacaggcgccttggcctggggcggggcaggtgctgatgagcattctcc	1600
Pro108	1084	-----	1083
Pro177	1601	tagctcttccaggcacctgctggacagggcaggctgggaacgctggggcc	1650
Pro108	1084	-----	1083
Pro177	1651	gagtggcagttccctccctactcagctgggtggcagccactggcctcacg	1700
Pro108	1084	-----	1083
Pro177	1701	gagcgccctgtggtctggagcgcattgctgggtcgtgggtcagggcctggt	1750
Pro108	1084	-----	1083

# REPLACEMENT SHEET

Figure 3D

Pro177	1751	ggctctgggtctctgggtctcacctgatatgggtgtgggacagtcagtgt	1800
Pro108	1084	-----	1083
Pro177	1801	aggccccagacaacagcggacttcagactttcccgaggaggaactggagc	1850
Pro108	1084	-----	1083
Pro177	1851	ccaccaacctggccatgggccccgtcgtcctccaccctccatgttgctgg	1900
Pro108	1084	-----	1083
Pro177	1901	ctggagttgaggcaggtacggggccgccccacacctgcccccaagccat	1950
Pro108	1084	-----	1083
Pro177	1951	gtggtagggacagatgtcgtcttgaggagcagcagtaattacaagcttac	2000
Pro108	1084	-----	1083
Pro177	2001	tgtcagccgtccctggaagcaagggccaggtcaggtcagacaggaggccg	2050
Pro108	1084	-----	1083
Pro177	2051	cctggctggcggaaccactccccagacagagactgtgccagtcctggg	2100
Pro108	1084	-----	1083
Pro177	2101	tccctcctcatttgggatgaactgggcctccctgtgccagcctcggtgct	2150
Pro108	1084	-----	1083
Pro177	2151	gccctgccagtgccaggttgggtcctcactcatttgtccacgcggat	2200
Pro108	1084	-----	1083
Pro177	2201	gccccattccaagcagatgtcccgagccacttacccaacaggcagacgt	2250
Pro108	1084	-----	1083
Pro177	2251	gccagcactgttcgtggtgtgcaactgggtctggcggaagagcccctcgt	2300
Pro108	1084	-----	1083
Pro177	2301	gggcagagggtccagagaggtgcggtttgccccacatttgggggcactgg	2350
Pro108	1084	-----	1083
Pro177	2351	gccacagtgggcaggggagcacgtggccagtgcctgggtctgccacgat	2400



# REPLACEMENT SHEET

Figure 3E

Pro108	1084	-----	1083
Pro177	2401	gtgggagttccaccaccacagggaacttgagcggcagctccggctcttacg	2450
Pro108	1084	-----	1083
Pro177	2451	tagaaaacgcgcaactccagtccttaggttggtgccgaggttgctatggtg	2500
Pro108	1084	-----	1083
Pro177	2501	ccatcccatcttgccgctcactctgcgactgtgcggagaaacgcaagtgc	2550
Pro108	1084	-----	1083
Pro177	2551	ccccgaagggtgggcgtggcctctgatgaatgcacacgttggtgggaggt	2600
Pro108	1084	-----	1083
Pro177	2601	ggcttccgtttggtacgaagcgctcttcacgcgagcggttcacctcggtct	2650
Pro108	1084	-----cagttccagaaacgccgctggactgcgaggtctcc	1118
Pro177	2651	cccctttgcttggtccagttccagaaacgccgctggactgcgaggtctcc	2700
Pro108	1119	ctgtggtcgtcctggggactgtgcggaggccactgtgggaggctcgggac	1168
Pro177	2701	ctgtggtcgtcctggggactgtgcggaggccactgtgggaggctcgggac	2750
Pro108	1169	caagagcaggactcgctacgtccgggtccagcccgccaacaacgggagcc	1218
Pro177	2751	caagagcaggactcgctacgtccgggtccagcccgccaacaacgggagcc	2800
Pro108	1219	cctgccccgagctcgaagaagaggctgagtgcgtccctgataactgcgtc	1268
Pro177	2801	cctgccccgagctcgaagaagaggctgagtgcgtccctgataactgcgtc	2850
Pro108	1269	taagaccagagccccgcagcccctgggg-cccccgagccatgggggtgc	1317
Pro177	2851	taagaccagagccccgcagcccctggggcccccgagccatgggggtgc	2900
Pro108	1318	gggggctcctgtgcaggctcatgctgcaggcggccga-ggcacaggggggt	1366
Pro177	2901	gggggctcctgtgcaggctcatgctgcaggcggccgagggcacaggggggt	2950
Pro108	1367	ttcgcgctgctcctgaccgcggtgaggccgcgcgaccatctctgcactg	1416
Pro177	2951	ttcgcgctgctcctgaccgcggtgaggccgcgcgaccatctctgcactg	3000

## REPLACEMENT SHEET

**Figure 3F**

Pro108	1417	aagggccctctggtggccggcacgggcattgggaaacagcctcctctt	1466
Pro177	3001	aagggccctctggtggccggcacgggcattgggaaacagcctcctctt	3050
Pro108	1467	cccaaccttgcttcttaggggcccccggtgtcccgctctgctctcagcctcc	1516
Pro177	3051	cccaaccttgcttcttaggggcccccggtgtcccgctctgctctcagcctcc	3100
Pro108	1517	tcctcctgcaggataaaagtcacccccagggtccagctactctaaattat	1566
Pro177	3101	tcctcctgcaggataaaagtcacccccagggtccagctactctaaattat	3150
Pro108	1567	ggtctccttataagttattgctgctccaggagattgtccttcacgtcca	1616
Pro177	3151	-gtctccttataagttattgctgctccaggagattgtccttcacgtcca	3199
Pro108	1617	ggggcctggctcccacgtggttgacagatacctcagacctggtgctctagg	1666
Pro177	3200	ggggcctggctcccacgtggttgacagatacctcagacctggtgctctagg	3249
Pro108	1667	ctgtgctgagcccactctcccgagggcgcatccaagcgggggcccacttga	1716
Pro177	3250	ctgtgctgagcccactctcccgagggcgcatccaagcgggggcccacttga	3299
Pro108	1717	gaagtgaataaatggggcggtttcggaagcgtcagtgtttccatgttatg	1766
Pro177	3300	gaagtgaataaatggggcggtttcggaagcgtcagtgtttccatgttatg	3349
Pro108	1767	gatctctctgcgtttgaataaagactatctctgttgctcac	1807
Pro177	3350	gatctctctgcgtttgaataaagactatctctgttgctcaaaaa	3393

This image shows a vertical strip of a document page. It contains a narrow column of text and a small table at the bottom.

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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### Figure 4

Aligned sequences: 2

# 1: PRO108.aa

# 2: PRO177.aa

```
# Matrix: EBLOSUM62
```

```
# Gap penalty: 100.0
```

```
# Extend penalty: 0.01
```

#####

PRO108.aa	1	MENPSPAAALGKALCALLLATLGAAGQPLGGESIC SARAPAKYSITFTGK	50
PRO177.aa	1	MENPSPAAALGKALCALLLATLGAAGQPLGGESIC SARAPAKYSITFTGK	50
PRO108.aa	51	WSQTAFPKQYPLFRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAE R	100
PRO177.aa	51	WSQTAFPKQYPLFRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAE R	100
PRO108.aa	101	GEAWALMKEIEAAGEALQSVHAVFSAPAVPSGTGQTSAELEVQRRHSLVS	150
PRO177.aa	101	GEAWALMKEIEAAGEALQSVHEVFSAPAVPSGTGQTSAELEVQRRHSLVS	150
PRO108.aa	151	FVVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYPYDAGTDSGFTFSSP	200
PRO177.aa	151	FVVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYPYDAGTDSGFTFSSP	200
PRO108.aa	201	NFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLVRLRQSPRA	250
PRO177.aa	201	NFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLRLRLRQSPRA	250
PRO108.aa	251	FIPPAPVLP SRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRLGTKS	300
PRO177.aa	251	FIPPAPVLP SRDNEIVDSASGNNGHTGHMGHTAAPNPATGRPPNPNLRL	298
PRO108.aa	301	RTRYVRVQPANNGSPCPELEEEEAECVPDNCV	331
PRO177.aa	299		298

Figure 5A

# REPLACEMENT SHEET

```

# Aligned_sequences: 2
# 1: PRO108.aa
# 2: PRO177.orf
# Matrix: EBLOSUM62
# Gap_penalty: 100.0
# Extend_penalty: 0.01
#=====

PRO108.aa      1                                     0
PRO177.orf     1 RCDSCTLFAVESILQGHSPPEERMKGGSRQYL RDSVLS DTHPQVTCV SQLT      50
PRO108.aa      1                                     0
PRO177.orf     51 RKLARMALCGHRVTAMLQGT CGGLGTQPPHSSGLCSQAPWPGAGQVLMSI    100
PRO108.aa      1                                     0
PRO177.orf    101 LLALPGTCWTGQAGNAGAEWQFPYSAGWQPLASRSACGLERIAGSWVRA    150
PRO108.aa      1                                     0
PRO177.orf    151 CWLWVSGSHLIWVWDSQCRPQT TADFRLSRGGTGAHQPGHGPRRPPPSML    200
PRO108.aa      1                                     0
PRO177.orf    201 LAGVEAGTGPPHTCPPSHVVGTDVVL RSSSNYKLTVSRPWKQGPGQVRQE    250
PRO108.aa      1                                     0
PRO177.orf    251 AAWLAGTTPQTETVPSPGSL LIWDELGLPVPASVLPLPSAGLGSSLICPR    300
PRO108.aa      1                                     0
PRO177.orf    301 GCPIPSRCPRATYPTGRRASTVRGVQLVWREEPLVGRGSREVRFAPHLGA    350
PRO108.aa      1                                     0
PRO177.orf    351 LGHSGQGSTWVPVPWVCHDVGVPPPQGLERQLRL LRRNAQLQSLGCVRGCY    400
PRO108.aa      1                                     MEN      3
...:
PRO177.orf    401 GAIPSCRSLCDCAEKRKCPRRVGVASDECTRWWEVASVCTKRLFTRAFTS    450
PRO108.aa      4 PSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQ    53
...:
PRO177.orf    451 VSPLL-----                        455
PRO108.aa     54 TAFPKQYPLFRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEA    103

```

## REPLACEMENT SHEET

**Figure 5B**

PRO177.orf	456	-----	455
PRO108.aa	104	WALMKEIEAAGEALQSVHAVFSAPAVPSGTGQTSAELEVQRRHSLVSFVV	153
PRO177.orf	456	-----	455
PRO108.aa	154	RIVPSPDWFGVDSLDCGDRWREQAALDLYPYDAGTDSGFTFSSPNFA	203
PRO177.orf	456	-----	455
PRO108.aa	204	TIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLVRLRQSPRAFIP	253
PRO177.orf	456	-----	455
PRO108.aa	254	PAPVLPSRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGR LGTKSRTR	303
		..	
PRO177.orf	456	-----GPVPETPLDCEVSLWSSWGLCGGHCGR LGTKSRTR	490
PRO108.aa	304	YVRVQPANNGSPCPELEEEEAECVPDNCV	331
PRO177.orf	491	YVRVQPANNGSPCPELEEEEAECVPDNCV	518